

## Appendix A



### Consensus #1

	10	20	30	40	50	60
BB1193DIVSeqIdNo10	LSLHLRVSPSSPFSSPLHNEALVSRDMA	SSGLEEK	AGLSTG	QNPAGEGGE		59
GI 4325324	ME	MDQTTKALSEL	MDSS	SAQDAGPR	-----	37
GenBank X94451	YD	-----	-----	-----	SSVST	8

### Consensus #1

	70	80	90	100	110	120
BB1193DIVSeqIdNo10	PQLSKNAK	KEERKKL	KEERKKNKA	AAA	SGKP	
GI 4325324	-SKNAKK	KEERKKR	KEERKKRKA	AAKQ	SKASS	118
GenBank X94451	P-LSKNAKK	KEERKKR	KEERKKRKA	AAVAA	DA	94

### Consensus #1

	130	140	150	160	170	180
BB1193DIVSeqIdNo10	LKALDSKATA	GVNPYPHKFP	PVGI	YRTLSE	GEKLTDVACLAGRIMNKR	
GI 4325324	LKYLA	AAEKA	YVSKY	YVSKY	YVSKY	178
GenBank X94451	LNIES	RESGI	NPYPHKFR	FITMS	SPFFITMS	154

## Appendix A

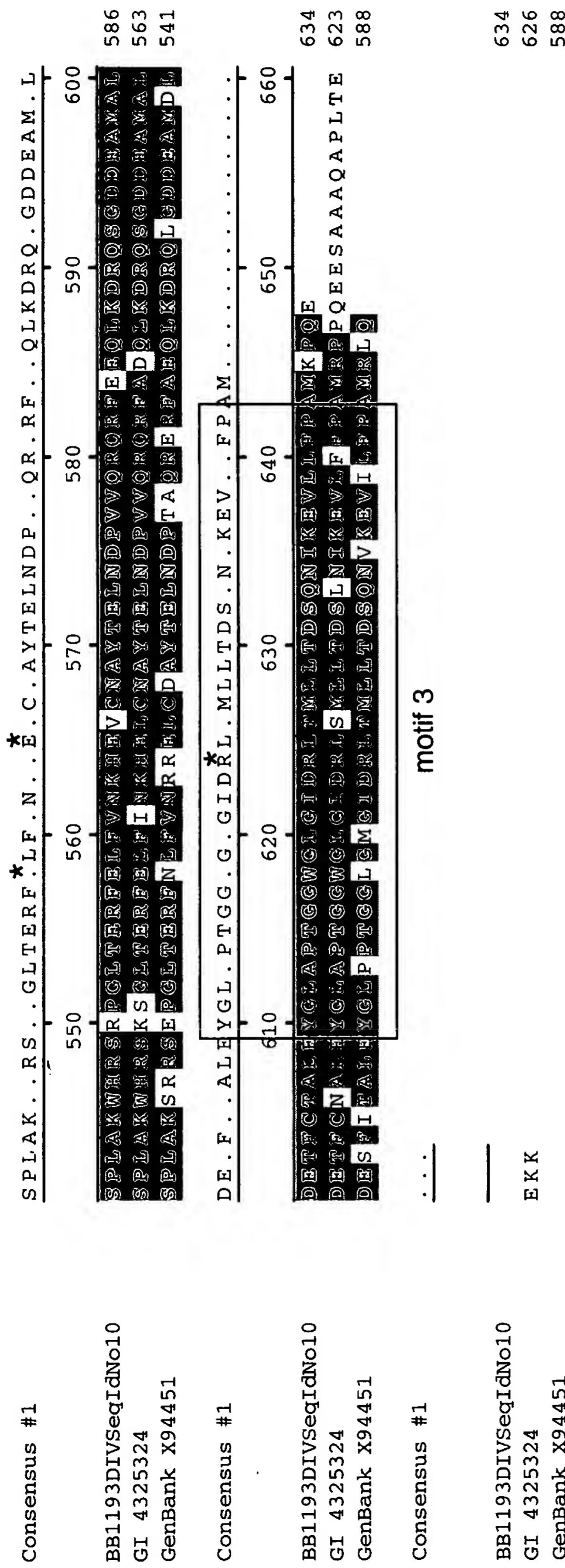
motif 1

# Appendix A

## motif 2

Consensus #1	N . L . . . R . . P E L Y L K . L . V G G	R V Y E . G K . F R N E G . D L T H . P E F T . C E . Y M A . A D Y	
	370	380	400
BB1193DIVSeqIdNo10	<b>N E L N M R I F M R I A P D L Y L K E L V V G G</b>	<b>D R V Y E I C K Q F R N E G I D T D Q H N P R</b>	
GI 4325324	<b>N D L M R L Y M R I A P D L Y L K Q L I V G G</b>	<b>D R V Y E I C K Q F R N E G I D T D Q H N P R</b>	406
GenBank X94451	<b>N E L D T E L I R V S P E L Y L K K L V V G G</b>	<b>D R V Y E I C K Q F R N E G I D T D Q H N P R</b>	383
			361
Consensus #1	N D L M . . T E . . L S G M V K . L T G . Y K I . Y . A N G . . . P I E I D F T P P F R . I . M . . . L E . . A . . .		
	430	440	450
BB1193DIVSeqIdNo10	<b>N D L M B L T E T M I I S C G M V K D L T G C Y K I K W H A N G V T N P D I E I D F T P P F R . I . M . . . L E . . A . . .</b>	<b>K D L E A M A N S S</b>	466
GI 4325324	<b>N D L M B M R E V M I I S C G M V K E L T G C Y K I K V N A N C Y D K D P I E I D F T P P F R . I . M . . . L E . . A . . .</b>	<b>E M I G E L E K W A K L N</b>	443
GenBank X94451	<b>N D L M D L T H Q L L S C G M V K D L T G C S Y K I R Y H A N C L D N E P I E I D F T P P F R . I . M . . . L E . . A . . .</b>	<b>K i D M L S E L E K W A N I S</b>	421
Consensus #1	I P . D L . S . . A N . . L . . . C . . . D V K C P P P . T T . R L I D K L V G . F . E . . C . N P T F I I N . P E I M		
	490	500	510
BB1193DIVSeqIdNo10	<b>I P K D L S S D E A N R Y L I E A C V K Y D V K C P P P Q T T S R L L D K L V G E F L E T C V N P T F I I N R P F I M</b>	<b>526</b>	
GI 4325324	<b>I P K D L A S E F A N K Y L I D A C A R F D V K C P P P Q T T A R L L D K L V G E F L E P T C V N P T F I I N Q P F I M</b>	<b>503</b>	
GenBank X94451	<b>I P R D L S S E S A N K H L V D V C E K F D V K C P P P H T T R L L D K L V G E F I E V N C I N P T F I I N R P F I M</b>	<b>481</b>	

## Appendix A



**Consensus #1:** When all match the residue on the Consensus show the residue of the Consensus, otherwise show ‘’.

**Shade** (with black at 40% fill) residues that match the Consensus named “Consensus #1” exactly.

The three highly conserved motifs (1, 2 and 3) are indicated by boxes. Residues which are important for substrate binding are indicated by asterisks.